

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 08:18:40 ; Search time 10 Seconds

(without alignments)  
503.354 Million cell updates/sec

Title: US-09-818-954A-1

Perfect score: 722

Sequence: 1 MKLAFLEIGPMALLLAGVG.....VAIRDCGACSTATTECEFI 130

Scoring table: BL0SUM62

Gapop 10.0 , Gapect 0.5

Searched: 105224 seqs, 38719550 residues

105224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213.5	29.6	149	1	GTH2_CLUPA
2	210	29.1	141	1	LSHB_BOVIN
3	209	28.9	140	1	GTH2_CARAU
4	209	28.9	144	1	GTH2_CYPCA
5	207	28.7	141	1	GTH2_HYPMO
6	207	28.7	146	1	GTH2_CTEID
7	204	28.3	138	1	GTH2_CLAGA
8	202.5	28.0	141	1	LSHB_SHEEP
9	201.5	27.9	140	1	GTH2_ANGAN
10	201	27.8	142	1	GTH2_ONCKE
11	199	27.6	136	1	GTH2_FUNHE
12	198	27.4	113	1	GTHB_MURCI
13	197	27.3	115	1	GTH2_THUOB
14	196	27.1	107	1	FSHB_RANCA
15	192	26.6	142	1	GTH2_ONMCA
16	189	26.2	112	1	LSHB_RANCA
17	189	26.2	139	1	GTH2_MORSA
18	186.5	25.8	142	1	GTH2_MORSA
19	186.5	25.8	169	1	LSHB_EOUBU
20	184.5	25.6	169	1	LSHB_EOUBU
21	184	25.5	142	1	GTH2_EDUAS
22	184	25.5	146	1	GTH2_ONCTS
23	183.5	25.5	169	1	GTH2_TRITC
24	181	25.1	137	1	LSHB_HORSE
25	180.5	25.0	141	1	GTH2_ACALA
26	178	24.7	141	1	LSHB_CERST
27	178	24.7	141	1	LSHB_CERST
28	176	24.4	141	1	LSHB_RAT
29	175	24.2	126	1	FSHB_TRIYU
30	175	24.2	141	1	FSHB_MOUSE
31	174	24.1	141	1	LSHB_MOUSE
32	173	24.0	138	1	LSHB_PIG
33	172.5	23.9	138	1	LSHB_MACRU
					LSHB_CANFA
					P188442 canis fam11

34	171	23.7	147	1	TSHB_ANGAN	Q08127 anguilla an
35	167	23.1	129	1	FSHB_CAYVO	Q91k69 cavia porce
36	165	22.9	118	1	LSHB_BALAC	P33088 bataeopter
37	164	22.7	128	1	LSHB_STRA	P80664 struthio ca
38	164	22.7	129	1	FSHB_HUMAN	P01225 homo sapien
39	164	22.7	129	1	FSHB_HUMAN	O46430 trichosurus
40	164	22.7	130	1	FSHB_MOUSE	Q60687 mus musculu
41	163.5	22.6	143	1	LSHB_FELCA	P7805 felis silve
42	163	22.6	130	1	FSHB_RAT	P18427 rattus norv
43	162	22.4	129	1	FSHB_PIG	P01228 sus scrofa
44	162	22.4	141	1	LSHB_HUMAN	P01229 homo sapien
45	161	22.3	118	1	LSHB_PHYCA	P25330 physeter ca

## ALIGNMENTS

RESULT 1	ID	GTH2_CLUPA	STANDARD:	PRT:	149 AA.
AC	Q9YGH2				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DE	Gonadotropin beta-II chain precursor (GTH-II-beta).				
OS	Clupea pallasii (Pacific herring).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;				
OC	Clupeinae; Clupea.				
OX	NCBI_TaxID=30724;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Plutitary;				
RA	Power M.E., Carlislefield J., Wallis G.P., Sherwood N.M.;				
RT	"Isolation and characterization of a cDNA for gonadotropin II-beta of				
RT	Pacific herring, an ancient teleost."				
RL	J. Fish Biol. 50:315-323(1997).				
CC	-1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.				
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.				
CC	-1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN				
CC	FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
CC	EMBL: X91984; CAA63038.1; -.				
CC	HSSP: P01233; IXL.				
CC	DR HSSP: P01233; IXL.				
CC	DR InterPro: IPR000359; Cys_Knot.				
CC	DR InterPro: IPR001545; Glyco_hormone_beta.				
CC	DR Pfam: PF00007; Cys_Knot; 1.				
CC	DR SMART: SM00068; GHB; 1.				
CC	DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.				
CC	DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.				
CC	DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.				
CC	KW Hormone; Glycoprotein; Signal.				
CC	FT SIGNAL	1	24		POTENTIAL.
CC	FT CHAIN	1	149		GONADOTROPIN BETA-II CHAIN.
CC	FT DISULFID	30	78		BY SIMILARITY.
CC	FT DISULFID	44	93		BY SIMILARITY.
CC	FT DISULFID	47	131		BY SIMILARITY.
CC	FT DISULFID	55	109		BY SIMILARITY.
CC	FT DISULFID	59	111		BY SIMILARITY.
CC	FT DISULFID	114	121		BY SIMILARITY.
CC	FT CARBOHYD	34	34		N-LINKED (GLCNAc...)(POTENTIAL).
CC	SO SEQUENCE	149 AA:	16627 MW:	4585DC6B34367069 CMC64:	
CC	Query Match	29.6%;	Score 213.5;	DB 1;	Length 149;
CC	Best Local Similarity	38.8%;	Pred. No. 3.2e-15;		
CC	Matches 47;	Conservative 18;	Mismatches 49;	Indels 7;	Gaps 4;

```

QY 10 PMALLTAGGCGVGC--ASSGQILRFECVAVAEFFFLAKKPGC-RGLRTITDAGCRRET 66
Db 5 PECTILLILCMKCVLAVPACQCFNLDP---CVLVNETVSYVEKEGCPCLVFRITICSGRPT 61
QY 67 WEKPILEPPYLEAHNRCTYNETKQVTKLPNCAQGVDPFYTYPAVIRDCGACSTATTE 126
Db 62 -KEPYRKSPFSVAVQHVCYTGNGFRYETIRLPDCAQGVDPVLYTYPAVALSCGSLCSMDTSD 120
QY 127 C 127
Db 121 C 121

RESULT 2
LSHB_BOVIN STANDARD: PRT; 141 AA.
AC P04651;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
  beta) (LSH-B) (LH-B).
GN LHB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85207729; PubMed=2987241;
RA Virgin J.B., Silver B.J., Thomson A.R., Nilsson J.H.;
RT "The gene for the beta subunit of bovine luteinizing hormone encodes
  a gonadotropin mRNA with an unusually short 5'-untranslated region.";
RL J. Biol. Chem. 260:7072-7077(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85182575; PubMed=3838746;
RA Maurer R.A.;
RT "Analysis of several bovine lutropin beta subunit cDNAs reveals
  heterogeneity in nucleotide sequence.";
RL J. Biol. Chem. 260:4684-4687(1985).
RN [3]
RP SEQUENCE OF 21-139.
RX MEDLINE=74075724; PubMed=4770795;
RA Maghain-Rogister G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from
  bovine and porcine species.";
RL Eur. J. Biochem. 39:235-253(1973).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
  THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
  CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
  LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
  FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M10077; AAA30623.1; -
DR EMBL; M1506; AAB59267.1; -
DR PIR; A01499; UTBOB.
DR HSSP; P01233; 1XUL.
DR GLYCOSITEDB; P04651; -
DR InterPro; IPR000359; Gys_knot.
DR InterPro; IPR002400; GF_gysknot.
DR

```

DR	InterPro:IPR001545; Glyco_hormone_beta.
DR	Pfam: PF00007; Cys_knot_1.
DR	PRINTS: PR00438; GFCYSKNOT.
DR	SMART: SM0068; GHY_1.
DR	PROSITE: PS00261; GLYCO_HORMONE_BETA_1.
DR	PROSITE: PS00689; GLYCO_HORMONE_BETA_2.
KM	Hormone; Signal; Glycoprotein.
FT	SIGNAL
FT	CHAIN
FT	DISEULFID
FT	DISEULFID
FT	DISEULFID
FT	DISEULFID
FT	DISEULFID
FT	CARBOHYD
FT	CONFLICT
FT	CONFLICT
FT	CONFLICT
FT	CONFLICT
SO	SEQUENCE
Query Match	Best Local Similarity
Matches	Conservative
OY	6 LELPMMALLLAGGVGVGASSGNLRRTFYVCAYREFFFLAKPKPCR-GLRTITPDACWGR
DB	3 MFGILLMLLIGVAG--VMASRGPLRL-CQPLNATLAERKEKCPICITFTTISICAGYC
OY	65 ETWER-PLEPPYEIAHHRVCTYNETRKQIVTKLPNCAGVDPEPTYTPVAIRCDGCACST
DB	59 PSMKRVLPIVILPMPQ--RVCTFHELRFAVRLPGCGPVDPMVSPPVALSCHCPCRL
OY	123 ATTEC
DB	116 STDTC
RESULT 3	
GTH2_CARAU	
ID	GTH2_CARAU STANDARD; PRT; 140 AA.
AC	Q98849;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Gonadotropin beta-II chain precursor (GTH-II-beta) [luteinizing hormone-like GTH].
OS	Carassius auratus (Goldfish).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopteleostei; Teleostei; Euteleostei; Ostariophysi;
OC	Cypriniformes; Cyprinidae; Carassius.
RX	NCB1_Taxid=7957;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUE=Pituitary;
RX	MEDLINE=97242868; PubMed=9073500;
RA	Yoshiura Y., Kobayashi M., Kato Y., Aida K.;
RT	"Molecular cloning of the cdnas encoding two gonadotropin beta subunits (GTH-I beta and -II beta) from the goldfish, Carassius auratus.";
RT	Gen. Comp. Endocrinol. 105:379-389(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Sohn Y.C., Yoshiura Y., Suetake H., Kobayashi M., Aida K.;
RT	"Nucleotide sequence of gonadotropin II beta subunit gene in goldfish.";
RT	Fisheries Sci. 65:800-801(1999).
CC	-I- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC	-1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN

```

RX MEDLINE/78124308; PubMed-607993;
RA JOLLES J., BURZAWA-GERARD E., FONTAINE Y.-A., JOLLES P.:
RT "The evolution of gonadotropins: some molecular data concerning a
RT non-mammalian pituitary gonadotropin, the hormone from a teleost
RT fish (Cyprinus carpio L.).";
RL Biochimie 59:893-898(1977).
CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X59888; CAA42542.1; -.
DR EMBL; X59889; CAA42543.1; -.
DR PIR; S29677; S29677.
DR PIR; S29678; S29678.
DR PIR; A01504; URCAB.
DR PIR; J70462; J70462.
DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Glyco_hormone_beta.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GREYSKNOT.
DR SMART; SM0068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 27
FT CHAIN 28 142 GONADOTROPIN BETA-II CHAIN.
FT PROPEP 143 144
FT DISULFID 33 81 BY SIMILARITY.
FT DISULFID 47 96 BY SIMILARITY.
FT DISULFID 50 134 BY SIMILARITY.
FT DISULFID 58 112 BY SIMILARITY.
FT DISULFID 62 114 BY SIMILARITY.
FT DISULFID 117 124 BY SIMILARITY.
FT CARBOHD 37 37 N-LINKED (GLCNAC...) (PROBABLE).
SO SEQUENCE 144 AA; 16039 MW; 854FE80DA39DCFB8 CRC64;

Query Match 28.9%; Score 209; DB 1; Length 144;
Best Local Similarity 42.5%; Pred. No. 8.9e-15;
Matches 37; Conservative 17; Mismatches 31; Indels 2; Gaps 2;

QY 42 TELAKPGCC-IGLRITTTACGRCGEETWEKPILEHHRVCTYNETKOVYKLRCA 100
DB 39 TVANEKECCPCVLVIQTTTICSGHCLT-KEPVYKSPFSTVYOHVCTYRDVRIETVRLPDCP 97
QY 101 PGVDPEFTYTPVAIRCDGAGCSTATTEC 127
DB 98 PGVDRIHTYTPVALSCDCSLCTMDTSDC 124

RESULT 5
GTH2_HYPMO STANDARD; PRT; 141 AA.
ID GTH2_HYPMO
AC P37038;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta) [luteinizing
DE hormone-like GTH].
OS Hypophthalmichthys molitrix (Silver carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Hypophthalmichthys.

```

```

OX NCBI_TaxID=13095;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=pituitary;
RX MEDLINE=90236229; PubMed=2332148;
RA Chang Y.S., Huang C.J., Huang F.-L., Liu C.S., Lo T.-B.;
RT "Purification, characterization, and molecular cloning of
gonadotropin subunits of silver carp (Hypophthalmichthys molitrix).";
RL Gen. Comp. Endocrinol. 78:23-33(1990).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
DR PIR: B60626; B60626.
DR HSSP: P01233; 1XUL.
DR Interpro: IPR000359; Cys_knot.
DR Interpro: IPR002400; GF_cysknot.
DR Interpro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot_1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GHb; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 139 GONADOTROPIN BETA-II CHAIN.
FT PROPEP 140 141
FT DISULFID 30 78 BY SIMILARITY.
FT DISULFID 44 93 BY SIMILARITY.
FT DISULFID 47 131 BY SIMILARITY.
FT DISULFID 55 109 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 114 121 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC...)(POTENTIAL).
SQ SEQUENCE 141 AA; 15856 MW; A42C48FE983EEA46 CRC64;

Query Match 28.7%; Score 207; DB 1; Length 141;
Best Local Similarity 42.5%; Pred. No. 1.4e-14;
Matches 37; Conservative 16; Mismatches 32; Indels 2; Gaps 2;

OY 42 TFLAKRPG-RGLRITTDACWGCETWEKPILEPPIEAHHRCTVNEKQTVKLPNCA 100
DB 36 TVAVEKEGCPKCLVFQTTICSGHCLT-KEPVYKSPSTVYQHVCYRDVYETVRLPDCP 94
OY 101 PGVDPFYTPVAIRCDCGACSTATTEC 127
DB 95 PGVDPHITFPVALSCDCSLCTMDTSDC 121

RESULT 6
ID GTH2_CTEID STANDARD; PRT; 146 AA.
AC P30984;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta) (Luteinizing
hormone-like GTH) (Fragment).
OS Gonadotropin gonad idella (Grass carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Ctenopharyngodon.
OX NCBI_TaxID=7959;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pituitary;
RA Chang Y.S., Huang F.-L., Lo T.-B.;
RL Submitted (Jul-1991) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X61051; CAA43385.1; -.
DR PIR: S16763; S16763.
DR HSSP: P01233; 1XUL.
DR Interpro: IPR000359; Cys_knot.
DR Interpro: IPR001345; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot_1.
DR SMART: SM00068; GHb; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal.
FT NON_TER 1 28
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 146 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 35 83 BY SIMILARITY.
FT DISULFID 49 98 BY SIMILARITY.
FT DISULFID 52 136 BY SIMILARITY.
FT DISULFID 60 114 BY SIMILARITY.
FT DISULFID 64 116 BY SIMILARITY.
FT DISULFID 119 126 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC...)(POTENTIAL).
SQ SEQUENCE 146 AA; 16320 MW; 65173444AC679082 CRC64;

Query Match 28.7%; Score 207; DB 1; Length 146;
Best Local Similarity 42.5%; Pred. No. 1.5e-14;
Matches 37; Conservative 16; Mismatches 32; Indels 2; Gaps 2;

OY 42 TFLAKRPG-RGLRITTDACWGCETWEKPILEPPIEAHHRCTVNEKQTVKLPNCA 100
DB 41 TVAVEKEGCPKCLVFQTTICSGHCLT-KEPVYKSPSTVYQHVCYRDVYETVRLPDCP 99
OY 101 PGVDPFYTPVAIRCDCGACSTATTEC 127
DB 100 PGVDPHITFPVALSCDCSLCTMDTSDC 126

RESULT 7
ID GTH2_CLAGA STANDARD; PRT; 138 AA.
AC P53543;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Clarias gariepinus (Sharptooth catfish) (African catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Clariidae; Clarias.
OX NCBI_TaxID=13013;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pituitary;
RA Rebers F.E.M., Tensen C.P., Schulz R.W., Goos H.J.T., Bogerd J.;
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 22-138.
RC TISSUE=pituitary;
RX MEDLINE=93051153; PubMed=1426937;
RA Koide Y., Noso T., Schouten G., Peute J., Zandbergen M.A., Bogerd J.,
Schulz R.W., Kawachi H., Goos H.J.;
RL "Maturational gonadotropin from the African catfish, Clarias
gariepinus: purification, characterization, localization, and
RT biological activity";
RL Gen. Comp. Endocrinol. 87:327-341(1997).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

```

CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X97761; CAA66359.1; -  
 DR HSP: P01233; 1XUL.  
 DR InterPro: IPR000359; Cys\_knot.  
 DR InterPro: IPR001545; Glyco\_hormone\_beta.  
 DR Pfam: PF00007; Cys\_knot; 1.  
 DR SMART: SM00068; GHb; 1.  
 DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 KW Hormone; Glycoprotein; signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 138 GONADOTROPIN BETA-II CHAIN.  
 FT DISULFID 27 75 BY SIMILARITY.  
 FT DISULFID 41 90 BY SIMILARITY.  
 FT DISULFID 44 128 BY SIMILARITY.  
 FT DISULFID 52 106 BY SIMILARITY.  
 FT DISULFID 56 108 BY SIMILARITY.  
 FT DISULFID 111 118 BY SIMILARITY.  
 FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 138 AA; 15772 MW; 670D81FAFAC6880E CRC64;  
 Query Match 28.3%; Score 204; DB 1; Length 138;  
 Best Local Similarity 40.2%; Pred. No. 2.8e-14;  
 Matches 33; Conservative 18; Mismatches 32; Indels 2; Gaps 2;  
 QY 42 TFLAKKRGCG-RLRITTDACWGRCETWEKPEPIEAEHHRVCTYNTKQVTKLPNCA 100  
 DB 33 TVSEYKGGCPKCLAFQGTSGHCFE-KEPYKSPFSSITGVHCTYRVRETRIRLPDCR 91  
 QY 101 PGVDPFTYTPAIRDCGACGACSTATTEC 127  
 DB 92 PGVDPHYTPVALSCSCLCTMDPDSDC 118  
 RESULT 8  
 LSHB\_SHEEP STANDARD; PRT; 141 AA.  
 ID LSHB\_SHEEP  
 AC P01231;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-  
 DE beta) (LSH-B) (LH-B) (interstitial cell stimulating hormone).  
 GN LHB.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OC NCBI\_taxid=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93351742; Pubmed=8349025.  
 RA Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;  
 RT "Characterization of the ovine LH beta-subunit gene: the promoter  
 RT directs gonadotrope-specific expression in transgenic mice.";  
 RL Mol. Cell. Endocrinol. 93:157-165(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=pituitary;  
 RA MEDLINE=90245669; Pubmed=2336396;  
 RA D'Angelo-Bernard G., Mounai M., Jutisz M., Counis R.;  
 RT "Cloning and sequence analysis of the cDNA for the precursor of the  
 RT beta subunit of ovine luteinizing hormone.";

RL Nucleic Acids Res. 18:2175-2175(1990).  
 RN [3]  
 RP SEQUENCE OF 21-139.  
 RX MEDLINE=7211145; Pubmed=4556309;  
 RA Liu W.-K., Nahm H.S., Sweeney C.M., Holcomb G.N., Ward D.N.;  
 RT "The primary structure of ovine luteinizing hormone. II. The amino  
 RT acid sequence of the reduced, S-carboxymethylated A-subunit (LH-  
 RT beta).";  
 RL J. Biol. Chem. 247:4365-4381(1972).  
 RN [4]  
 RP SEQUENCE OF 21-139.  
 RX MEDLINE=73190035; Pubmed=4575435;  
 RA Sairam M.R., Samy T.S.A., Pakkoff H., Li C.H.;  
 RT "The primary structure of ovine interstitial cell-stimulating  
 RT hormone. II. The beta-subunit.";  
 RL Arch. Biochem. Biophys. 153:572-586(1972).  
 RN [5]  
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
 RX MEDLINE=76068152; Pubmed=1201911;  
 RA Chung D., Sairam M.R., Li C.H.;  
 RT "The primary structure of ovine interstitial cell stimulating  
 RT hormone. IV: Disulfide bridges of the beta subunit.";  
 RL Int. J. Pept. Protein Res. 7:487-493(1975).  
 RN [6]  
 RP STRUCTURE OF CARBOHYDRATE.  
 RX MEDLINE=91061170; Pubmed=2209620;  
 RA Weisshar G., Hiyama J., Renwick A.G.C.;  
 RT "Site-specific N-glycosylation of ovine lutropin. Structural analysis  
 RT by one- and two-dimensional 1H-NMR spectroscopy.";  
 RL Eur. J. Biochem. 192:741-751(1990).  
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: S64695; AAB27819.1; -  
 DR EMBL: X52488; CAA36729.1; -  
 DR PIR: A01500; UTSMB.  
 DR PIR: S09232; S09232.  
 DR HSP: P01233; 1XUL.  
 DR GLYCOSULEDB: P01231; -  
 DR InterPro: IPR000359; Cys\_knot.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001545; Glyco\_hormone\_beta.  
 DR Pfam: PF00007; Cys\_knot; 1.  
 DR PRINTS: PR00438; GFCTSKNOT.  
 DR SMART: SM00068; GHb; 1.  
 DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 KW Hormone; signal; Glycoprotein.  
 FT SIGNAL 1 20  
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.  
 FT DISULFID 29 77 BY SIMILARITY.  
 FT DISULFID 43 92 BY SIMILARITY.  
 FT DISULFID 46 130 BY SIMILARITY.  
 FT DISULFID 54 108 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 113 120 BY SIMILARITY.  
 FT MOD\_RES 21 21 BLOCKED.  
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).  
 FT VARIANT 138 141 /FTID-CAR.000046.  
 FT MISSING (IN SOME MOLECULES).

```

FT CONFLICT 30 30 O -> E (IN REF. 4).
FT CONFLICT 59 59 L -> P (IN REF. 1).
FT CONFLICT 63 63 R -> Q (IN REF. 2).
FT CONFLICT 71 72 PM -> PPM (IN REF. 4).
FT CONFLICT 81 81 E -> Q (IN REF. 4).
FT CONFLICT 122 123 GP -> PG (IN REF. 3 AND 4).
FT CONFLICT 126 126 Q -> E (IN REF. 3 AND 4).
SO SEQUENCE 141 AA; 15184 MM; C59EC7C0AA55A9DC CRC64;

Query Match 28.0%; Score 202.5; DB 1; Length 141;
Best Local Similarity 39.2%; Pred. No. 4.1e-14;
Matches 47; Conservative 19; Mismatches 45; Indels 9; Gaps 5;

QY 11 MALLLAGYGCVLGASSNLRFTVCACAREFFFLKPKGCR-GLRITTDACWGRCETWEK 69
Db 7 LLLMALLCAGVQ-WMSRGLRPL--CQPINATLAAKEKCPVCTFTTSGAGYCLSKMR 63
QY 70 --PILEPPYIEAHNVCTYNETKYVTKLIPNCAPEVDPEPTYTPVALRCDGACSTATTEK 127
Db 64 VLPVILPPMPQ--RVCTYHELRFSAFVRLPGCPGVDPMVSPVALSCHGCPRLSLTDC 120

RESULT 9
GTH2_ANGAN
ID GTH2_ANGAN STANDARD: PRT; 140 AA.
AC P27767;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguillidae; Anguilla.
OX NCBI_TaxID=7936;
RN [1]
RP SEQUENCE FROM N.A..
RA TISSUE=Pituitary;
RC MEDLINE=90334703; PubMed=2116136;
RX Querat B., Moummi M., Jutisz M., Fontaine Y.A., Counis R.;
RT "Molecular cloning and sequence analysis of the cDNA for the putative
RL beta subunit of the type-II gonadotropin from the European eel.";
CC J. Mol. Endocrinol. 4:257-264(1990).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its use
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/1sb.ch).
```

```

FT DISULFID 55 109 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 114 121 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 140 AA: 15478 MW: 10312.506171/DD80 CRC64:

Query Match 27.9%; Score 211.5; DB 1; Length 140;
Best Local Similarity 38.9%; Pred. No. 5.2e-14;
Matches 42; Conservative 16; Mismatches 47; Indels 3; Gaps 3;

QY 21 CVLGASSGNLRTFVGCAGAREFTFLAKRPGC-NGLRITTDACMGRCETWEKPILEPPYIEA 79
Dd 16 CHILVSAGS-SLLLECEPINFETISYEKGDCPCICLWFOTISICGHCT-KDPSYKSPILSTV 73
QY 80 HHRATYNTNETKQVTKALPNCARGVDPFPYTHVAIHGDCAGCATATTEC 127
Dd 74 YORCTTYRDVRYETRYALPDCRGVDPHYTFYALSCDCLMTDTSDC 121

RESULT 10
GTH2_ONCKE
AC ID GTH2_ONCKE STANDARD; PRT; 142 AA.
AC P10256;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta) .
OS Oncorhynchus keta (Chum salmon) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteocephali; Cyprinodontiformes; Salmonidae; Oncorhynchus.
RX NCBI_TaxID=8018;
RX 11
RX RP SEQUENCE FROM N.A.
RX RA MEDLINE=90046849; PubMed=2813416;
RX RA Sekine S., Saito A., Itoh H., Kawachi H., Itoh S.;
RT "Molecular cloning and sequence analysis of chum salmon gonadotropin
RT cDNAs."
RT Proc. Natl. Acad. Sci. U.S.A. 86:8645-8649(1989).
RN 121
RN RP SEQUENCE OF 24-142.
RX RA MEDLINE=89053031; PubMed=3192067;
RX RA Itoh H., Suzuki K., Kawachi H.;
RT "The complete amino acid sequences of beta-subunits of two distinct
RT chum salmon GTHs."
RL Gen. Comp. Endocrinol. 71:438-451(1983).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib.ch.)
CC -----
CC EMBL: M27154; AAA49409.1; -
DR PIR: C36179; C36179.
DR HSSP: P01233; 1XUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFcysKNOT.
DR SMART: SMO0068; GHb; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 142 GONADOTROPIN BETA-II CHAIN.

```

```

FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
FT VARIANT 73 73 Y -> I.
FT VARIANT 86 86 T -> K.
SQ SEQUENCE 142 AA: 15872 MW: E3IE117DA235C486 CRC64:

Query Match 27.8%; Score 201; DB 1; Length 142;
Best Local Similarity 34.7%; Pred. No. 5.9e-14;
Matches 42; Conservative 19; Mismatches 44; Indels 16; Gaps 3;

QY 22 VLGASSGMLRTFVGCAYNE-----FTFLAKKPGCC-RGLRTTDDACMGRCET 66
Db 1 MGLHVTGLISLFLCTLLEPEVSGSIMOPCQPINQTVLSLEKCGCPCLVIOFPGICSGHCYT 60
QY 67 WEKPILEPPYLEAHHRCTYNETKQVTKLPCNCAFGVDPFYTPVAIRDCGACSTATTE 126
Db 61 KEPEFKSPFSTVYVQHVCTYRDVRYETRLPDCPPWVDEHVTYPAALSCDCSLCNMDTSD 119
QY 127 C 127
Db 120 C 120

RESULT 11
GTH2_FUNHE
ID GTH2_FUNHE STANDARD: PRT; 136 AA.
AC P30972:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pituitary;
RA MEDLINE=92405806; PubMed=1526312;
RA Lin Y.-W.P., Rupnow B.A., Price D.A., Greenberg R.M., Wallace R.A.;
RT "Fundulus heteroclitus gonadotropins. 3. Cloning and sequencing of
RT gonadotropic hormone (GTH) I and II beta-subunits using the
RT polymerase chain reaction.";
RL Mol. Cell. Endocrinol. 85:127-139(1992).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M87015; AAB59963.1; -.
CC HSSP; P01233; 1XUL.
CC InterPro: IPR000359; Cys_knot.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR001545; Glyco_hormone_beta.
CC Pfam; PF00007; Cys_knot; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC SMART; SM00068; GHB; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.

```

```

DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 136 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 27 75 BY SIMILARITY.
FT DISULFID 41 90 BY SIMILARITY.
FT DISULFID 44 128 BY SIMILARITY.
FT DISULFID 52 106 BY SIMILARITY.
FT DISULFID 56 108 BY SIMILARITY.
FT DISULFID 111 118 BY SIMILARITY.
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 136 AA: 15016 MW: 716576844A6A1653 CRC64:

Query Match 27.6%; Score 199; DB 1; Length 136;
Best Local Similarity 41.9%; Pred. No. 9.1e-14;
Matches 39; Conservative 12; Mismatches 40; Indels 2; Gaps 2;

QY 36 CAVREFFFLAKKPGCGRL-RITTDACWRCGFEMERPILEPPYLEAHHRCTYNETKQVTV 94
Db 27 COLLNQTLSLEKRGSGCGCHRVETTTCSGYCAT-KDPNKTYSNKAIGHVCTYGDLYKTF 85
QY 95 KLPNCAPGVDPFYTPVAIRDCGACSTATTTC 127
Db 86 EFPECVPGVDPVVTYPPVALSCRCGCGCATMTSDC 118

RESULT 12
GTHB_MURCI
ID GTHB_MURCI STANDARD: PRT; 113 AA.
AC P12837:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Gonadotropin beta chain.
OS Murænesox cinereus (Pike eel) (Daggeetooth pike conger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Congridae;
OC Murænesocidae; Murænesox.
OX NCBI_TaxID=7946;
RN [1]
RP SEQUENCE.
RC TISSUE=pituitary;
RX MEDLINE=90092087; PubMed=2598923;
RA Liu C.-S., Huang F.-L., Chang Y.-S., Lo T.-B.;
RT "Pike eel (Murænesox cinereus) gonadotropin. Amino acid sequences of
RT both alpha and beta subunits.";
RL Eur. J. Biochem. 186:105-114(1989).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
CC PIR; S07092; S07092.
CC HSSP; P01233; 1XUL.
CC InterPro: IPR000359; Cys_knot.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR001545; Glyco_hormone_beta.
CC Pfam; PF00007; Cys_knot; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC SMART; SM00068; GHB; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone: Glycoprotein.
FT DISULFID 6 54 BY SIMILARITY.
FT DISULFID 20 69 BY SIMILARITY.
FT DISULFID 23 107 BY SIMILARITY.
FT DISULFID 31 85 BY SIMILARITY.
FT DISULFID 35 87 BY SIMILARITY.
FT DISULFID 90 97 BY SIMILARITY.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 113 AA: 12582 MW: 17DDDADE6AC6F7 CRC64:

Query Match 27.4%; Score 198; DB 1; Length 113;
Best Local Similarity 42.5%; Pred. No. 9.6e-14;

```

	Matches	37,	Conservative	14;	Mismatches	34;	Indels	2;	Gaps	2;
Oy	42	TFLAKKPGC-KGLRTTTDACMGRCTEWEKPLEPYIEAHNRVCYNETKYATKLPNCA	100							
Dd	12	TTSVGEQCPKCLVPOTSSCSGHCHT-KDPSXKSPLSITVYGVCYRVDYRETVRLPDCR	70							
Oy	101	PGVDPFYYPVALIRGDCGACSTATTEC	127							
Dd	71	PGVDHVTFPVALSCDNLTMDTSDC	97							
<hr/>										
RESULT_13										
ID	PTH2_THUOB	STANDARD:	PRT:	115 AA.						
AC	p37206;									
DT	01-OCT-1994 (Rel. 30, Created)									
DT	01-OCT-1994 (Rel. 30, Last sequence update)									
DT	16-OCT-2001 (Rel. 40, Last annotation update)									
DE	Gonadotropin beta-II chain (GNH-II-beta).									
OS	Thunnus obesus (Bigeye tuna).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;									
CC	Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;									
CC	Acanthomorphae; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;									
OX	Scombridae; Thunnus.									
NL	NCBI_TaxID=8241;									
RN	[1]									
RP	SEQUENCE.									
RC	TISSUE=Pituitary;									
TX	MEDLINE=94186287; PubMed=8138353;									
RA	Kawada T., Kawazoe I., Kimura S., Sasamoto Y., Alda K., Kawachi H.;									
RT	"Identification and characterization of gonadotropin I and II from pituitary glands of tuna (Thunnus obesus)."									
RU	Int. J. Pept. Protein Res. 43:69-80(1994).									
RL	- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.									
CC	- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.									
CC	- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.									
DR	HSEP; P01233; 1XUL.									
DR	InterPro: IPRO00359; Cys_knot.									
DR	InterPro: IPR002400; GF_cysknot.									
DR	InterPro: IPR001545; Glyco_hormone_beta.									
DR	Pfam: PF00007; Cys_knot; 1.									
DR	PRINTS: PR00438; GFCYSKNKT.									
DR	SMART: SM00041; CT; 1.									
DR	SMART: SM00068; GHF; 1.									
DR	PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.									
DR	PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.									
KW	Hormone; Glycoprotein.									
FT	DISULFD	6	54		BY SIMILARITY.					
FT	DISULFD	20	69		BY SIMILARITY.					
FT	DISULFD	23	107		BY SIMILARITY.					
FT	DISULFD	31	85		BY SIMILARITY.					
FT	DISULFD	35	87		BY SIMILARITY.					
FT	DISULFD	90	97		BY SIMILARITY.					
FT	CARBOND	10	10		N-LINKED (GLCNAG..).					
SO	SEQUENCE	115 AA;	12992 MW;	8721CI07836F5CAE9 CR064;						
<hr/>										
Query Match		27.3%; Score 197; DB 1; Length 115;								
Best Local Similarity		38.7%; Pred. No.1,2e-13;								
Matches		36;	Conservative	17;	Mismatches	36;	Indels	2;	Gaps	2;
Oy	36	CAVEREFETLAKKPGRGRLR-IITTDACMGRCETWEKPDLPEPYIEAHNRVCYTNETKYATV	94							
Dd	6	COLIJNTSVSEKEGCASHPVFETTICSGHCIT-KDPVIKIIPRSKVYQHNVCTYRDFFYKKRF	64							
Oy	95	KLPNCAPGVDPPTTYTPVAIRCDCGACSTATTEC	127							
Dd	65	ELPDPCPGVDPIPTYTPVALSCHCGRCAMDTSDC	97							
<hr/>										
RESULT_14										
ID	FSHB_RANCA	STANDARD:	PRT:	107 AA.						

[illegible]



```

RA Kato Y., Gen K., Maruyama O., Tomizawa K., Kato T.;
RT "Molecular cloning of cDNAs encoding two gonadotrophin beta subunits
RT (GPH-I beta and -II beta) from the masu salmon, Oncorhynchus masou;
RT rapid divergence of the GPH-I beta gene.";
RL J. Mol. Endocrinol. 11:275-282(1993).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S69276; AAB30424.1; -.
DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Glyco_hormone_beta.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
DR KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 142 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 142 AA; 15884 MW; 70A3906EAB3EFF CRC64;

Query Match 26.6%; Score 192; DB 1; Length 142;
Best Local Similarity 33.9%; Pred. No. 5e-13;
Matches 41; Conservative 18; Mismatches 46; Indels 16; Gaps 3;

QY 22 VLGASSGNLRTFVGCARE-----FTFLAKKRC-RGLRITTDACWRCET 66
Db 1 MLGLHVGTLISLCLILEPEVGSIMOPCPINQTFVSLKRGCPCLVIQTPICSGHCIT 60
QY 67 WEKPILEPPYIEAHHRVCTYNKQVTKLPNCAGPVDPEYTYPAIRCDGAGCSTATTE 126
Db 61 -KEPYFRSPFSTVYOHVCTYDVRTEMIRLPDCPPWVDPHTYVALSCDCLCMNDTSD 119
QY 127 C 127
Db 120 C 120

```

Search completed: October 11, 2002, 08:23:07  
 Job time : 11 secs

**THIS PAGE BLANK (USPTO)**